



SEQUENCE LISTING

<110> Duvick, Jonathan P.
Gilliam, Jacob T.
Maddox, Joyce R.
Crasta, Oswald R.
Folkerts, Otto

<120> Amino Polyol Amine Oxidase
Polynucleotides and Related Polypeptides and Methods of Use

<130> 0875C

<140> 09/770,564

<141> 2001-01-26

<150> US 60/092,936

<151> 1998-07-15

<150> US 09/352,168

<151> 1999-07-12

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 372

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> misc_feature

<222> (346)...(346)

<223> n = A,T,C or G

<400> 1

```
gggccccggc gttctcgtag gctgcgcgga gttgggtccca gacagacttt tgtcgtacct 60
gcttggactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc 120
attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatgggggtca cagctcgatt 180
ggaggacgcc cgagaagcct tggtcgcgcc accacggctt gtcccatacg aagactatct 240
tgctatagta gccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg 300
gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc 360
ggaacacggc gc                                     372
```

<210> 2

<211> 182

<212> DNA

<213> *Exophiala spinifera*

<400> 2
gaattttccg ccaatgcttg cttctcggcg ggaagagggtg gtgaaaatgt caaggtggga 60
tacaagggtg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc 120
gatcgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc 180
ac 182

<210> 3
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 3' RACE, N21965

<400> 3
tggtttcgtt accgacaacc ttgtatccc 29

<210> 4
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 5' RACE, N21968

<400> 4
gagttggtcc cagacagact tttgtcgt 28

<210> 5
<211> 1389
<212> DNA
<213> *Exophiala spinifera*

<220>
<221> CDS
<222> (1)...(1386)

<400> 5
gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg 48
Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
1 5 10 15
gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
20 25 30
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp

50	55	60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag			240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu			
65	70	75	80
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac			288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp			
	85	90	95
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag			336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu			
	100	105	110
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc			384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile			
	115	120	125
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg			432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg			
	130	135	140
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg			480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu			
145	150	155	160
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt			528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly			
	165	170	175
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag			576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys			
	180	185	190
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg			624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly			
	195	200	205
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg			672
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met			
	210	215	220
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct			720
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala			
225	230	235	240
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc			768
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly			
	245	250	255
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg			816
Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu			
	260	265	270

tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca	864
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	
275 280 285	
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta	912
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val	
290 295 300	
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa	960
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln	
305 310 315 320	
tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
325 330 335	
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
340 345 350	
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
355 360 365	
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
370 375 380	
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga	1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	
385 390 395 400	
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg	1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser	
405 410 415	
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg	1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr	
420 425 430	
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa	1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln	
435 440 445	
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
450 455 460	
tag	1389
<210> 6	
<211> 462	

<212> PRT

<213> *Exophiala spinifera*

<400> 6

Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu
1				5					10					15	
Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu
			20					25					30		
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly
		35					40					45			
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp
	50					55					60				
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu
65					70					75					80
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp
				85					90					95	
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu
			100					105					110		
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile
		115					120					125			
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg
	130					135					140				
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu
145					150					155					160
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly
				165					170					175	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
			180					185					190		
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly
		195					200					205			
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met
	210					215					220				
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala
225					230					235					240
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly
				245					250					255	
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu
			260					265					270		
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala
		275					280					285			
Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val
	290					295					300				
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln
305					310					315					320
Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val
				325					330					335	
Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg
			340					345					350		
Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp
		355					360					365			
Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro
	370					375					380				
Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly

385		390		395		400									
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser
			405					410						415	
Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr
			420					425						430	
Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln
		435					440					445			
Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala		
	450					455					460				

<210> 7
 <211> 1442
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS
 <222> (1)...(646)

<221> intron
 <222> (647)...(699)

<221> CDS
 <222> (700)...(1439)

<400> 7	
gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg	48
Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu	
1 5 10 15	
gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	

100										105										110										
gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	384														
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile															
115					120					125																				
gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	432														
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg															
130					135					140																				
ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	480														
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu															
145					150					155					160															
cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggg	528														
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly															
165					170					175																				
gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	576														
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys															
180					185					190																				
agt	gcc	acc	ggg	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	624														
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly															
195					200					205																				
cag	tat	gtg	cga	tgc	aaa	aca	g	gtgcgtgtgg	tgctcgtctca	ggg	gggggac	676																		
Gln	Tyr	Val	Arg	Cys	Lys	Thr																								
210					215																									
tcgtttctca	gtgggtcattc	cag	gt	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	728																	
										Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser											
										220					225															
aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	776														
Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu															
230					235					240																				
att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	824														
Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala															
245					250					255																				
gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	872														
Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr															
260					265					270																				
ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	920														
Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu															
275					280					285																				
gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	968														
Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp															
290					295					300					305															

gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg	1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
310 315 320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp	
325 330 335	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag	1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys	
340 345 350	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa	1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln	
355 360 365	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc	1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala	
370 375 380 385	
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct	1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala	
390 395 400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg	1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala	
405 410 415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct	1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser	
420 425 430	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga	1400
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg	
435 440 445	
ggg gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1442
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
450 455 460	

<210> 8

<211> 462

<212> PRT

<213> *Exophiala spinifera*

<400> 8

Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu	
1 5 10 15	
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	

<210> 9
 <211> 458
 <212> PRT
 <213> Exophiala spinifera

<400> 9

Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu
1				5					10					15	
Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu
			20					25					30		
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly
		35					40					45			
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp
	50					55					60				
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu
65					70					75					80
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp
				85				90						95	
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu
			100					105					110		
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile
		115					120					125			
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg
	130					135					140				
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu
145					150					155					160
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly
				165				170						175	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
		180					185					190			
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly
		195				200						205			
Gln	Tyr	Val	Arg	Cys	Lys	Thr	Gly	Ala	Cys	Gly	Val	Val	Ser	Gly	Gly
	210					215					220				
Gly	Leu	Val	Ser	Gln	Trp	Ser	Phe	Gln	Val	Cys	Ser	Arg	Phe	Ala	Met
225					230					235					240
Pro	Cys	Gln	Arg	Asn	Leu	Phe	Gln	Ala	Gln	Cys	Thr	Ser	Thr	Pro	Pro
				245				250						255	
Ser	Leu	Lys	Leu	Ser	Ser	Arg	His	Pro	Ala	Val	Gln	Tyr	Asp	Arg	Pro
			260				265						270		
Arg	Ala	Pro	Cys	Ser	Glu	Ala	Lys	Arg	Trp	Trp	Phe	Arg	Tyr	Arg	Gln
		275					280					285			
Pro	Cys	Ile	Pro	Pro	His	Phe	His	His	Leu	Phe	Pro	Pro	Arg	Ser	Lys
	290					295					300				
His	Trp	Arg	Lys	Ile	Leu	Ser	Trp	Ala	Thr	Ile	Ala	Arg	Ser	Ser	Tyr
305					310					315					320
Gly	Thr	Ser	Arg	Gly	Gly	Ala	Asn	Lys	Ala	Ser	Arg	Ala	Ser	Ser	Asn
				325				330					335		
Arg	Ala	Val	Thr	Pro	Ser	His	Leu	Pro	Glu	Ile	Pro	Ala	Ser	Thr	Ser
			340				345					350			
Ile	Asp	Asn	Gly	Pro	Leu	Pro	Val	Ser	Trp	Ser	Glu	Thr	Arg	Asp	Gly

```

          355          360          365
Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
   370          375          380
Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
385          390          395          400
Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
          405          410          415
Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
          420          425          430
Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu
          435          440          445
Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr
   450          455

```

```

<210> 10
<211> 1392
<212> DNA
<213> Exophiala spinifera

```

```

<220>
<221> CDS
<222> (1)...(1389)

<221> misc_feature
<222> (1)...(3)
<223> Extra lysine in K:trAPAO

```

```

<400> 10
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
  1          5          10          15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
          20          25          30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
          35          40          45

ggg ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
  50          55          60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
  65          70          75          80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
          85          90          95

```

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg gtt gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	1389
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
450 455 460	
tag	1392
<210> 11	
<211> 463	
<212> PRT	
<213> <i>Exophiala spinifera</i>	
<220>	
<221> VARIANT	
<222> (1)...(1)	
<223> Extra lysine in the polypeptide sequence of K:trAPAO.	

<400> 11

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	1	5	10	15
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	20	25	30	
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	35	40	45	
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	50	55	60	
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	65	70	75	
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	85	90	95	
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	100	105	110	
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	115	120	125	
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	130	135	140	
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	145	150	155	
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	165	170	175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	180	185	190	
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	195	200	205	
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	210	215	220	
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	225	230	235	
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	245	250	255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	260	265	270	
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	275	280	285	
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	290	295	300	
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	305	310	315	
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	325	330	335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	340	345	350	
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	355	360	365	
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	370	375	380	
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	385	390	395	
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	405	410	415	

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 12
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23256

<400> 12
 ggggaattca aagacaacgt tgcggacgtg gtag 34

<210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23259

<400> 13
 ggggcggccg cctatgctgc tggcaccagg ctac 34

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
 tggtttcggt accgacaacc ttgtatccc 29

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 5' race, N21968

<400> 15

gagttggtcc cagacagact tttgtcgt

28

<210> 16

<211> 1673

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> sig_peptide

<222> (1)...(267)

<223> yeast alpha mating factor secretion signal

<221> CDS

<222> (1)...(1662)

<400> 16

atg	aga	ttt	cct	tca	att	ttt	act	gct	gtt	tta	ttc	gca	gca	tcc	tcc	48
Met	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser	
			-85						-80					-75		

gca	tta	gct	gct	cca	gtc	aac	act	aca	aca	gaa	gat	gaa	acg	gca	caa	96
Ala	Leu	Ala	Ala	Pro	Val	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln	
		-70						-65					-60			

att	ccg	gct	gaa	gct	gtc	atc	ggg	tac	tca	gat	tta	gaa	ggg	gat	ttc	144
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe	
	-55						-50					-45				

gat	gtt	gct	gtt	ttg	cca	ttt	tcc	aac	agc	aca	aat	aac	ggg	tta	ttg	192
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu	
	-40					-35					-30					

ttt	ata	aat	act	act	att	gcc	agc	att	gct	gct	aaa	gaa	gaa	ggg	gta	240
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val	
-25					-20				-15					-10		

tct	ctc	gag	aaa	aga	gag	gct	gaa	gct	gaa	ttc	aaa	gac	aac	gtt	gcg	288
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Glu	Phe	Lys	Asp	Asn	Val	Ala	
			-5					1					5			

gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggg	ttg	gag	acg	gca	cgc	336
Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	
		10					15					20				

aaa	gtc	cag	gcc	gcc	ggg	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	384
Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	
	25					30					35					

cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggg	ccc	ggc	agg	acg	432
Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	
	40				45				50					55		

act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	480
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser		
				60					65					70			
gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	528	
Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln		
			75					80					85				
agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	576	
Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr		
		90					95					100					
aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	ggt	gca	agt	gca	624	
Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala		
	105					110					115						
ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	672	
Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser		
120					125				130						135		
ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg	720	
Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val		
				140				145						150			
agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	768	
Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu		
			155					160					165				
ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	gtg	gaa	gcc	cac	816	
Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His		
		170					175					180					
gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggt	864	
Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly		
	185					190					195						
ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	912	
Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg		
200					205				210					215			
tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	960	
Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu		
				220				225						230			
gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	1008	
Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln		
			235					240					245				
tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	1056	
Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg		
		250					255					260					
agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	1104	
Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu		

265	270	275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat			1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn			
280	285	290	295
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg			1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro			
	300	305	310
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac			1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			
	315	320	325
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg			1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			
	330	335	340
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa			1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			
	345	350	355
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
	360	365	370
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
	380	385	390
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala			
	395	400	405
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg			1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr			
	410	415	420
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg			1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp			
	425	430	435
aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca			1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala			
	440	445	450
gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c			1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala			
	460	465	

<210> 17
<211> 554

Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
 265 270 275
 Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
 280 285 290 295
 Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
 300 305 310
 Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
 315 320 325
 Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
 330 335 340
 Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
 345 350 355
 Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
 360 365 370 375
 Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
 380 385 390
 Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
 395 400 405
 Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
 410 415 420
 Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
 425 430 435
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
 440 445 450 455
 Glu Val Val Ala Ser Leu Val Pro Ala Ala
 460 465

<210> 18
 <211> 2079
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(2076)
 <223>

<221> misc_feature
 <222> (1)...(687)
 <223> gst fusion + polylinker

<221> misc_feature
 <222> (688)...(2076)
 <223> K:trAPAO

<221> misc_feature
 <222> (688)...(690)
 <223> Extra lysine

<223> GST:K:trAPAO fusion for bacterial expression.

<400> 18

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	

acg	ttt	ggt	ggt	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	gtt	ccg	cgt	672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
gga	tcc	ccg	gaa	ttc	aaa	gac	aac	gtt	gcg	gac	gtg	gta	gtg	gtg	ggc	720
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	
225					230					235					240	
gct	ggc	ttg	agc	ggt	ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggt	768
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	
				245					250					255		
ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	816
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	
			260					265					270			
ctg	agc	gta	caa	tcg	ggt	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	864
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	
		275					280					285				
gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	912
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	
	290					295					300					
gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	960
Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	
305					310					315					320	
atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	1008
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	
				325					330					335		
tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	1056
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	
			340					345					350			
gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	1104
Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	
		355					360					365				
agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	1152
Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	
	370					375					380					
gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	1200
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	
385					390					395					400	
aca	cgc	gct	ctg	ctc	ggt	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	1248
Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	
				405					410					415		

ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg	1296
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
420 425 430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
435 440 445	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
450 455 460	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
515 520 525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc	1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
530 535 540	
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga	1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
545 550 555 560	
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
565 570 575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	
580 585 590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg	1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	
595 600 605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag	1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	
610 615 620	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat	1920

Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	
625					630					635					640	
ctc	atc	aca	ctg	ggt	tcg	gcg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	1968
Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	
				645					650					655		
ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	2016
Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	
				660				665					670			
gcc	ata	cga	tcg	ggt	caa	cga	ggt	gct	gca	gaa	gtt	gtg	gct	agc	ctg	2064
Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	
			675				680					685				
gtg	cca	gca	gca	tag												2079
Val	Pro	Ala	Ala													
				690												

<210> 19
 <211> 692
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GST:K:trAPAO; GST + linker, aa 1-229; K:trAPAO, aa 230-692. Translation of SEQ ID NO: 18.

<400>	19															
Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5				10						15		
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70					75					80	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165					170						175	

Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	180	185	190
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	195	200	205
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	210	215	220
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	225	230	235
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	245	250	255
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	260	265	270
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	275	280	285
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	290	295	300
Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	305	310	315
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	325	330	335
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	340	345	350
Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	355	360	365
Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	370	375	380
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	385	390	395
Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	405	410	415
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	420	425	430
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	435	440	445
Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	450	455	460
Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	465	470	475
Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	485	490	495
Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	500	505	510
Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	515	520	525
Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	530	535	540
Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	545	550	555
Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	565	570	575
Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	580	585	590
Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly			

```

      595              600              605
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
      610              615              620
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
      625              630              635              640
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
      645              650              655
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
      660              665              670
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
      675              680              685
Val Pro Ala Ala
      690

```

```

<210> 20
<211> 1464
<212> DNA
<213> Artificial Sequence

```

```

<220>
<221> sig_peptide
<222> (1)...(72)
<223> Barley Alpha Amylase signal sequence

```

```

<221> misc_feature
<222> (73)...(1464)
<223> K:trAPAOcDNA

```

```

<221> CDS
<222> (1)...(1461)

```

```

<221> misc_feature
<222> (73)...(75)
<223> Added lysine residue

```

```

<223> Nucleotide sequence of K:trAPAO translational
      fusion with barley alpha amylase signal sequence,
      for expression and secretion of the mature trAPAO
      in maize.

```

```

<400> 20
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc 48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
      -20              -15              -10

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta 96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
      -5              1              5

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag 144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
      10              15              20

```

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg	192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly	
25 30 35 40	
gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac	240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn	
45 50 55	
gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc	288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser	
60 65 70	
aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act	336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr	
75 80 85	
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct	384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro	
90 95 100	
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa	432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu	
105 110 115 120	
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac	480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp	
125 130 135	
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg	528
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala	
140 145 150	
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca	576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala	
155 160 165	
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc	624
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser	
170 175 180	
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat	672
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn	
185 190 195 200	
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca	720
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr	
205 210 215	
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc	768
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly	
220 225 230	

tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tcg	gca	tcc	816
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	
		235					240					245				
ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	agc	aaa	aag	864
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	
	250					255					260					
gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	tca	912
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	
265					270					275					280	
cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	tct	atc	ctg	960
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	
				285					290					295		
ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	cgc	1008
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	
			300					305					310			
gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	tca	1056
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	
		315					320					325				
ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	acc	1104
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	
	330					335					340					
tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	aag	1152
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	
345					350					355					360	
cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	gcc	tac	gag	1200
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	
				365				370						375		
aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	gag	1248
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	
			380					385					390			
tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	ggg	1296
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	
		395					400					405				
ctg	aac	gat	ctc	atc	aca	ctg	ggg	tcg	gcg	ctc	aga	acg	ccg	ttc	aag	1344
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	
	410					415					420					
agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	aaa	ggg	tat	1392
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	
425					430				435						440	
atg	gaa	ggg	gcc	ata	cga	tcg	ggg	caa	cga	ggg	gct	gca	gaa	gtt	gtg	1440

Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
445 450 455

gct agc ctg gtg cca gca gca tag
Ala Ser Leu Val Pro Ala Ala
460

1464

<210> 21
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<221> SIGNAL
<222> (1)...(24)

<223> K:trAPAO translational fusion with barley alpha
amylase signal sequence, for expression and
secretion of the mature trAPAO in maize.

<400> 21
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
-20 -15 -10
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
-5 1 5
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
10 15 20
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
25 30 35 40
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
45 50 55
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
60 65 70
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
75 80 85
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro
90 95 100
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
105 110 115 120
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
125 130 135
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
140 145 150
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
155 160 165
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
170 175 180
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
185 190 195 200
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
205 210 215

Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
 220 225 230
 Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
 235 240 245
 Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
 250 255 260
 Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
 265 270 275 280
 Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
 285 290 295
 Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
 300 305 310
 Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
 315 320 325
 Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
 330 335 340
 Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
 345 350 355 360
 Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
 365 370 375
 Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
 380 385 390
 Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
 395 400 405
 Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
 410 415 420
 Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
 425 430 435 440
 Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
 445 450 455
 Ala Ser Leu Val Pro Ala Ala
 460

<210> 22
 <211> 1803
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS
 <222> (1)...(1800)

<400> 22
 atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca 48
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1 5 10 15

 gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg 96
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30

 aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct 144

Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro		
		35					40					45					
gcc	tac	gag	aaa	cag	gtt	gcc	caa	gca	ttc	gcc	aat	ctg	cga	gct	tgc	192	
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys		
	50					55					60						
ctt	gct	gca	gtt	gga	gcc	act	tca	aac	gac	gtc	acc	aag	ctc	aat	tac	240	
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr		
	65				70					75					80		
tac	atc	gtc	gac	tac	gcc	ccg	agc	aaa	ctc	acc	gca	att	gga	gat	ggg	288	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly		
			85						90					95			
ctg	aag	gct	acc	ttt	gcc	ctt	gac	agg	ctc	cct	cct	tgc	acg	ctg	gtg	336	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val		
		100						105				110					
cca	gtg	tcg	gcc	ttg	tct	tca	cct	gaa	tac	ctc	ttt	gag	gtt	gat	gcc	384	
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala		
	115						120					125					
acg	gcg	ctg	gtg	ccg	gga	cac	acg	acc	cca	gac	aac	gtt	gcg	gac	gtg	432	
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val		
	130				135						140						
gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggc	ttg	gag	acg	gca	cgc	aaa	gtc	480	
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val		
	145				150					155					160		
cag	gcc	gcc	ggc	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	528	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val		
			165						170					175			
ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggc	ccc	ggc	agg	acg	act	atc	576	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile		
		180						185					190				
aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	624	
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val		
		195					200					205					
tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	672	
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr		
	210					215					220						
act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggc	aca	acc	act	aca	gct	720	
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala		
	225				230					235					240		
cct	tat	ggc	gac	tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg	768	
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala		

245										250					255					
gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	816				
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln					
			260					265					270							
gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg	agc	ttc	864				
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe					
		275					280					285								
gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	912				
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val					
	290					295				300										
gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggc	gtg	gaa	gcc	cac	gag	atc	960				
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile					
305					310				315					320						
agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggc	ctc	agt	1008				
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser					
			325						330				335							
aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	1056				
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys					
		340					345					350								
aca	ggc	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	gtt	cca	1104				
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro					
	355					360				365										
ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tcg	gca	1152				
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala					
	370				375				380											
tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	agc	aaa	1200				
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys					
385					390				395					400						
aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	1248				
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe					
			405					410					415							
tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	tct	atc	1296				
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile					
		420					425					430								
ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	1344				
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp					
		435				440					445									
cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	1392				
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile					
	450					455					460									

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485 490 495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500 505 510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
515 520 525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530 535 540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc	1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545 550 555 560	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
565 570 575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt	1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
580 585 590	
gtg gct agc ctg gtg cca gca gca tag	1803
Val Ala Ser Leu Val Pro Ala Ala	
595 600	

<210> 23

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 23

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1 5 10 15	
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	

65					70					75				80
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp Gly
				85					90					95
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu Val
			100					105					110	
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp Ala
		115					120					125		
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp Val
	130					135						140		
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys Val
145					150					155				160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg Val
				165					170					175
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr Ile
			180					185					190	
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu Val
	195						200					205		
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg Thr
	210					215						220		
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr Ala
225					230					235				240
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu Ala
				245					250					255
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu Gln
			260					265					270	
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser Phe
	275						280					285		
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly Val
	290					295					300			
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu Ile
305					310					315				320
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu Ser
				325					330					335
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys Lys
			340					345					350	
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val Pro
	355						360					365		
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser Ala
	370					375						380		
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser Lys
385					390					395				400
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr Phe
				405					410					415
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser Ile
			420					425					430	
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp Trp
	435						440					445		
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro Ile
	450					455						460		
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser Ile
465					470					475				480
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln Ser
				485					490					495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 24
 <211> 3003
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence is a barley alpha amylase signal
 sequence: espl mat: an artificial spacer sequence
 and K:trAPAO

<221> sig_peptide
 <222> (1)...(72)
 <223> Barley alpha amylase signal sequence

<221> misc_feature
 <222> (73)...(1575)
 <223> espl mat

<221> misc_feature
 <222> (1576)...(1611)
 <223> spacer sequence

<221> misc_feature
 <222> (1612)...(3000)
 <223> K:trAPAO

<221> CDS
 <222> (1)...(3000)

<221> misc_feature
 <222> (1612)...(1614)
 <223> Extra lysine

<400> 24
 atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc 48
 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly

	-20		-15		-10		
ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct	96						
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala							
	-5		1		5		
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc	144						
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr							
	10		15		20		
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt	192						
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe							
	25		30		35		40
gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act	240						
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr							
		45		50		55	
gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc	288						
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu							
		60		65		70	
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt	336						
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly							
		75		80		85	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag	384						
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu							
		90		95		100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa	432						
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu							
	105		110		115		120
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc	480						
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala							
		125		130		135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg	528						
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu							
		140		145		150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg	576						
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly							
		155		160		165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca	624						
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala							
		170		175		180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg	672						
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala							
	185		190		195		200

ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca	720
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro	
205 210 215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc	768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	
220 225 230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc	816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu	
235 240 245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat	864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	
250 255 260	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag	912
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu	
265 270 275 280	
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc	960
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	
285 290 295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc	1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala	
300 305 310	
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat	1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr	
315 320 325	
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt	1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu	
330 335 340	
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag	1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln	
345 350 355 360	
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc	1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile	
365 370 375	
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac	1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr	
380 385 390	
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg	1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val	
395 400 405	

tac	cac	agc	tct	gaa	gtc	ggg	atg	gtg	ttt	ggc	acg	tat	cct	gtc	gca	1344
Tyr	His	Ser	Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala	
	410					415					420					
agt	gcg	acc	gcc	ttg	gag	gcc	cag	acg	agc	aaa	tac	atg	cag	ggt	gcc	1392
Ser	Ala	Thr	Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala	
425					430					435					440	
tgg	gcg	gcc	ttt	gcc	aaa	aac	ccc	atg	aat	ggg	cct	ggg	tgg	aaa	caa	1440
Trp	Ala	Ala	Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys	Gln	
				445					450					455		
gtg	ccg	aat	gtc	gcg	gcg	ctt	ggc	tca	cca	ggc	aaa	gcc	atc	cag	gtt	1488
Val	Pro	Asn	Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val	
			460					465					470			
gac	gtc	tct	cca	gcg	aca	ata	gac	caa	cga	tgt	gcc	ttg	tac	acg	cgt	1536
Asp	Val	Ser	Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg	
		475					480					485				
tat	tat	act	gag	ttg	ggc	aca	atc	gcg	ccg	agg	aca	ttt	ggc	gga	ggc	1584
Tyr	Tyr	Thr	Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly	Gly	
	490					495					500					
agc	ggc	gga	ggc	agc	ggc	gga	ggc	agc	aaa	gac	aac	gtt	gcg	gac	gtg	1632
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp	Val	
505					510					515					520	
gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggt	ttg	gag	acg	gca	cgc	aaa	gtc	1680
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	
				525					530					535		
cag	gcc	gcc	ggt	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	1728
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	
			540					545					550			
ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggt	ccc	ggc	agg	acg	act	atc	1776
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	
		555					560					565				
aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	1824
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	
	570					575					580					
tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	1872
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	
585					590					595					600	
act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	aca	gct	1920
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	
				605					610					615		
cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg	1968

Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala		
			620					625					630				
gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	2016	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln		
		635					640					645					
gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg	agc	ttc	2064	
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe		
	650					655					660						
gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	2112	
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val		
665					670				675						680		
gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggg	gtg	gaa	gcc	cac	gag	atc	2160	
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile		
				685					690					695			
agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggg	ctc	agt	2208	
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser		
		700						705					710				
aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	2256	
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys		
		715					720					725					
aca	ggg	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	gtt	cca	2304	
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro		
	730					735					740						
ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tcg	gca	2352	
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala		
745					750				755						760		
tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	agc	aaa	2400	
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys		
			765						770					775			
aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	2448	
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe		
			780					785					790				
tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	tct	atc	2496	
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile		
		795					800					805					
ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	2544	
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp		
	810					815					820						
cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	2592	
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile		

825	830	835	840	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att				2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	845	850	855	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc				2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	860	865	870	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac				2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	875	880	885	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc				2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	890	895	900	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat				2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	905	910	915	920
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc				2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	925	930	935	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg				2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	940	945	950	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt				2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	955	960	965	
gtg gct agc ctg gtg cca gca gca tag				3003
Val Ala Ser Leu Val Pro Ala Ala	970	975		

<210> 25

<211> 1000

<212> PRT

<213> Artificial Sequence

<220>

<221> SIGNAL

<222> (1)...(24)

<223> translation of the BAA:ESP1:K:trAPAO construct
sequence of SEQ ID NO: 24

<400> 25

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly

				-20					-15					-10			
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala		
			-5					1				5					
Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr		
	10					15					20						
Val	Ser	Glu	Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe		
25					30				35						40		
Ala	Pro	Pro	Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr	Pro	Leu	Gln	Ala	Thr		
				45					50					55			
Ala	Tyr	Gly	Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu	Leu		
			60					65					70				
Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala	Gly		
	75						80					85					
Glu	Ser	Glu	Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu		
	90					95					100						
Asn	Thr	Asn	Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu		
105					110					115					120		
Tyr	Gly	Trp	Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala		
				125					130					135			
Asn	Gln	Asp	Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu		
			140					145					150				
Gly	Phe	Pro	Ala	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu	Gly		
		155					160					165					
Phe	Leu	Asp	Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala		
	170					175					180						
Ala	Phe	Gly	Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala		
185					190					195					200		
Gly	Gly	Arg	Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro		
				205					210					215			
Pro	Phe	Arg	Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe		
			220					225					230				
Pro	Lys	Gly	Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu		
		235					240					245					
Asn	Cys	Thr	Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp		
	250					255					260						
Leu	Ala	Thr	Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu		
265					270				275						280		
Tyr	Thr	Leu	Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg		
				285					290					295			
Thr	Thr	Gly	Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala		
			300					305					310				
Asn	Asp	Gly	Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr		
		315					320					325					
Leu	Glu	Glu	Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu		
	330					335					340						
Gly	Ala	Tyr	Pro	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp	Gln		
345					350					355					360		
Ile	Ala	Ala	Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile		
				365					370					375			
Val	Ala	Gln	Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr		
			380					385					390				
Tyr	Asn	Ala	Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val		
		395					400					405					

Tyr	His	Ser	Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala	410	415	420
Ser	Ala	Thr	Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala	425	430	435
Trp	Ala	Ala	Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys	Gln	445	450	455
Val	Pro	Asn	Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val	460	465	470
Asp	Val	Ser	Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg	475	480	485
Tyr	Tyr	Thr	Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly	Gly	490	495	500
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp	Val	505	510	515
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	525	530	535
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	540	545	550
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	555	560	565
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	570	575	580
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	585	590	595
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	605	610	615
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	620	625	630
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	635	640	645
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	650	655	660
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	665	670	675
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	685	690	695
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	700	705	710
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	715	720	725
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	730	735	740
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	745	750	755
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	765	770	775
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	780	785	790
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	795	800	805
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	810	815	820
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile			

825		830		835		840									
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile
				845				850						855	
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser
			860					865					870		
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr
		875					880				885				
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile
	890					895					900				
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr
905				910				915						920	
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe
			925				930						935		
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly
		940					945					950			
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val
	955					960					965				
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala								
	970				975										

<210> 26
 <211> 2976
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Barley alpha amylase signal sequence: BEST1
 mature: artificial spacer: and K:trAPAO. For
 plant expression.

<221> sig_peptide
 <222> (1)...(72)
 <223> Barley alpha amylase signal sequence

<221> mat_peptide
 <222> (73)...(1545)
 <223> BEST1 mature

<221> misc_feature
 <222> (1546)...(1584)
 <223> Artificial spacer sequence

<221> misc_feature
 <222> (1585)...(2973)
 <223> K:trAPAO

<221> CDS
 <222> (1)...(2973)

<221> misc_feature
 <222> (1585)...(1587)

<223> Extra lysine

<400> 26

atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc	48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly	
-20 -15 -10	
ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc	96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr	
-5 1 5	
gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc	144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg	
10 15 20	
gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg	192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro	
25 30 35 40	
ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt	240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe	
45 50 55	
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc	288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala	
60 65 70	
ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca	336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	
75 80 85	
ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc	384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	
90 95 100	
ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg	432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	
105 110 115 120	
ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac	480
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	
125 130 135	
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc	528
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	
140 145 150	
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg	576
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg	
155 160 165	
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg	624
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	

170	175	180	
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu 185 190 195 200			672
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser 205 210 215			720
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser 220 225 230			768
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro 235 240 245			816
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp 250 255 260			864
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu 265 270 275 280			912
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val 285 290 295			960
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly 300 305 310			1008
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala 315 320 325			1056
cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp 330 335 340			1104
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn 345 350 355 360			1152
cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln 365 370 375			1200
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly 380 385 390			1248

aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg	1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val	
395 400 405	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc	1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro	
410 415 420	
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc	1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val	
425 430 435 440	
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct	1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro	
445 450 455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc	1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg	
460 465 470	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc	1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly	
475 480 485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc	1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser	
490 495 500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
505 510 515 520	
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
525 530 535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
540 545 550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
555 560 565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
570 575 580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
585 590 595 600	

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
605 610 615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
620 625 630	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
635 640 645	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	2064
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
650 655 660	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	2112
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
665 670 675 680	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	2160
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
685 690 695	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	2208
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
700 705 710	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	2256
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
715 720 725	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	2304
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
730 735 740	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	2352
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
745 750 755 760	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	2400
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
765 770 775	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	2448
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
780 785 790	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	2496
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
795 800 805	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	2544

Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu		
810						815					820						
caa	tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	2592	
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp		
825					830				835						840		
gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	2640	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly		
				845					850					855			
cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	2688	
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp		
			860					865					870				
gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	2736	
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu		
			875				880					885					
ccg	gcc	aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	2784	
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln		
	890					895					900						
gga	gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	2832	
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly		
905					910					915					920		
tcg	gcg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	2880	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu		
				925					930					935			
acg	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggg	2928	
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly		
			940				945						950				
caa	cga	ggg	gct	gca	gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca		2973	
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala			
		955					960					965					
tag																	2976
<210> 27																	
<211> 991																	
<212> PRT																	
<213> Artificial Sequence																	
<220>																	
<221> SIGNAL																	
<222> (1)...(24)																	
<223> Translation of the BAA:BEST1:K:trAPAO construct																	
sequence of SEQ ID NO: 26																	

Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly
				-20						-15				-10	
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Thr	Asp	Phe	Pro	Val	Arg	Arg	Thr
			-5					1				5			
Asp	Leu	Gly	Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg
	10					15					20				
Gly	Ile	Pro	Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro
25					30					35					40
Pro	Gln	His	Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe
			45						50					55	
Gly	Ser	Asp	Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala
			60					65					70		
Pro	Gly	Val	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser
		75					80					85			
Gly	Ala	Lys	Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly
						95					100				
Gly	Phe	Ala	Gly	Gly	Thr	Ala	Ala	Met	Pro	Tyr	Tyr	Asp	Gly	Glu	Ala
105					110						115				120
Leu	Ala	Arg	Gln	Gly	Val	Val	Val	Val	Thr	Phe	Asn	Tyr	Arg	Thr	Asn
				125										135	
Ile	Leu	Gly	Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr
			140					145					150		
Gly	Thr	Ser	Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg
		155					160					165			
Trp	Val	Gln	Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val
	170					175					180				
Thr	Val	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu
185					190					195					200
Thr	Ser	Pro	Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser
			205						210				215		
Pro	Gly	Leu	Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser
			220					225					230		
Gly	Glu	Arg	Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro
		235					240					245			
Ala	Thr	Leu	Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp
	250					255					260				
Leu	Arg	Arg	Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu
265					270					275					280
Pro	Gln	Thr	Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val
			285						290					295	
Arg	Val	Leu	Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly
			300					305					310		
Arg	Ala	Pro	Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala
		315						320				325			
Gln	Phe	Gly	Asp	Gln</											

Arg	Ala	Pro	Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	395	400	405
Phe	Lys	Leu	Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	410	415	420
Thr	Pro	Ala	Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	425	430	435
Arg	Phe	Ala	Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	445	450	455
Ala	Tyr	Ser	Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	460	465	470
Ala	Ala	Val	Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	475	480	485
Ala	Lys	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	490	495	500
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	505	510	515
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	525	530	535
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	540	545	550
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	555	560	565
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	570	575	580
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	585	590	595
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	605	610	615
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	620	625	630
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	635	640	645
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	650	655	660
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	665	670	675
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	685	690	695
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	700	705	710
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	715	720	725
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	730	735	740
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	745	750	755
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	765	770	775
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	780	785	790
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	795	800	805
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu			

810		815		820
Gln Ser Ser Cys Asp Pro	Ile Ser Phe Ala Arg	Asp Thr Ser Ile Asp		
825	830	835	840	
Val Asp Arg Gln Trp Ser	Ile Thr Cys Phe Met	Val Gly Asp Pro Gly		
	845	850	855	
Arg Lys Trp Ser Gln Gln	Ser Lys Gln Val Arg	Gln Lys Ser Val Trp		
	860	865	870	
Asp Gln Leu Arg Ala Ala	Tyr Glu Asn Ala Gly	Ala Gln Val Pro Glu		
	875	880	885	
Pro Ala Asn Val Leu Glu	Ile Glu Trp Ser Lys	Gln Gln Tyr Phe Gln		
	890	895	900	
Gly Ala Pro Ser Ala Val	Tyr Gly Leu Asn Asp	Leu Ile Thr Leu Gly		
905	910	915	920	
Ser Ala Leu Arg Thr Pro	Phe Lys Ser Val His	Phe Val Gly Thr Glu		
	925	930	935	
Thr Ser Leu Val Trp Lys	Gly Tyr Met Glu Gly	Ala Ile Arg Ser Gly		
	940	945	950	
Gln Arg Gly Ala Ala Glu	Val Val Ala Ser Leu	Val Pro Ala Ala		
	955	960	965	

<210> 28
 <211> 3618
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> gst:espl:sp:K:trAPAO. For bacterial expression.

<221> CDS
 <222> (1)...(3615)

<221> misc_feature
 <222> (1)...(687)
 <223> gast + polylinker

<221> mat_peptide
 <222> (688)...(2190)
 <223> espl mat

<221> misc_feature
 <222> (2191)...(2226)
 <223> spacer sequence

<221> misc_feature
 <222> (2227)...(3615)
 <223> K:trAPAO

<221> misc_feature
 <222> (2227)...(2229)
 <223> Extra lysine

<400> 28

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	

acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg	720
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val	
225 230 235 240	
gtc ggc acg act act act gtc ccc ggc acc act gcg acc gtc agc gag	768
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu	
245 250 255	
ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct	816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	
260 265 270	
act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt	864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly	
275 280 285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc cgt gag att	912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile	
290 295 300	
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag	960
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu	
305 310 315 320	
gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac	1008
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn	
325 330 335	
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg	1056
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp	
340 345 350	
aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc aat cag gat	1104
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp	
355 360 365	
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct	1152
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	
370 375 380	
gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac	1200
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp	
385 390 395 400	
caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc	1248
Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly	
405 410 415	
ggc gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga	1296

Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala	Gly	Gly	Arg		
			420					425					430				
agt	gtc	gac	gtc	ctc	ttg	acg	tct	atg	cca	cac	aac	cca	ccc	ttc	cga	1344	
Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro	Pro	Phe	Arg		
		435					440					445					
gca	gca	atc	atg	gag	tcc	ggg	gtg	gct	aac	tac	aac	ttc	ccc	aag	gga	1392	
Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe	Pro	Lys	Gly		
	450					455					460						
gat	ttg	tcc	gaa	cct	tgg	aac	acc	act	gtt	caa	gct	ctc	aac	tgt	acc	1440	
Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu	Asn	Cys	Thr		
465					470					475					480		
acc	agt	atc	gac	atc	ttg	agt	tgt	atg	aga	aga	gtc	gat	ctc	gcc	act	1488	
Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp	Leu	Ala	Thr		
			485						490					495			
ctg	atg	aac	acg	atc	gag	caa	ctc	gga	ctt	ggg	ttt	gag	tac	acg	ttg	1536	
Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu	Tyr	Thr	Leu		
			500					505					510				
gac	aac	gta	acg	gct	gtg	tac	cgt	tct	gaa	acg	gct	cgc	acg	act	ggg	1584	
Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg	Thr	Thr	Gly		
		515					520					525					
gac	att	gct	cgt	gta	cct	gtt	ctc	gtc	ggg	acg	gtg	gcc	aac	gac	gga	1632	
Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala	Asn	Asp	Gly		
	530					535					540						
ctt	ctc	ttt	gtc	ctc	ggg	gag	aat	gac	acc	caa	gca	tat	ctc	gag	gag	1680	
Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr	Leu	Glu	Glu		
	545				550				555						560		
gca	atc	ccg	aat	cag	ccc	gac	ctt	tac	cag	act	ctc	ctt	gga	gca	tat	1728	
Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu	Gly	Ala	Tyr		
				565					570					575			
ccc	att	gga	tcc	cca	ggg	atc	gga	tcg	cct	caa	gat	cag	att	gcc	gcc	1776	
Pro	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp	Gln	Ile	Ala	Ala		
			580					585					590				
att	gag	acc	gag	gta	aga	ttc	cag	tgt	cct	tct	gcc	atc	gtg	gct	cag	1824	
Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile	Val	Ala	Gln		
		595					600					605					
gac	tcc	cgg	aat	cgg	ggg	atc	cct	tct	tgg	cgc	tac	tac	tac	aat	gcg	1872	
Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr	Tyr	Asn	Ala		
	610					615					620						
acc	ttt	gag	aat	ctg	gag	ctt	ttc	cct	ggg	tcc	gaa	gtg	tac	cac	agc	1920	
Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val	Tyr	His	Ser		

625	630	635	640	
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc				1968
Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr	645	650	655	
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc				2016
Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala	660	665	670	
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat				2064
Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn	675	680	685	
gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct				2112
Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser	690	695	700	
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act				2160
Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr	705	710	715	720
gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga				2208
Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly	725	730	735	
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg				2256
Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val	740	745	750	
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc				2304
Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala	755	760	765	
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag				2352
Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys	770	775	780	
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc				2400
Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu	785	790	795	800
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg				2448
Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu	805	810	815	
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat				2496
Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn	820	825	830	
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt				2544
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly	835	840	845	

gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc	2592
Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu	
850 855 860	
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag	2640
Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys	
865 870 875 880	
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac	2688
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr	
885 890 895	
tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag	2736
Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln	
900 905 910	
atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt	2784
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu	
915 920 925	
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc	2832
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe	
930 935 940	
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg	2880
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met	
945 950 955 960	
cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg	2928
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val	
965 970 975	
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt	2976
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys	
980 985 990	
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg	3024
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val	
995 1000 1005	
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct	3072
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro	
1010 1015 1020	
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac	3120
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr	
1025 1030 1035 1040	
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa	3168
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln	
1045 1050 1055	

ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc	3216
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala	
1060 1065 1070	
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc	3264
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe	
1075 1080 1085	
atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta	3312
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val	
1090 1095 1100	
cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc	3360
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala	
1105 1110 1115 1120	
ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg	3408
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser	
1125 1130 1135	
aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac	3456
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn	
1140 1145 1150	
gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt	3504
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val	
1155 1160 1165	
cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa	3552
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu	
1170 1175 1180	
ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc	3600
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser	
1185 1190 1195 1200	
ctg gtg cca gca gca tag	3618
Leu Val Pro Ala Ala	
1205	

<210> 29

<211> 1205

<212> PRT

<213> Artificial Sequence

<220>

<223> Translation of the GST:ESPl:K:trAPAO fusion
sequence for bacterial expression as provided in
SEQ ID NO: 28

<400> 29

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

1				5				10					15			
Thr	Arg	Leu	Leu	Glu	Tyr	Leu	Glu	Lys	Tyr	Glu	Glu	His	Leu			
			20				25					30				
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70					75					80	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
	115						120					125				
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165					170					175		
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210				215						220					
Gly	Ser	Pro	Glu	Phe	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala	Gly	Met	Val	
225					230					235					240	
Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr	Val	Ser	Glu	
				245					250					255		
Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe	Ala	Pro	Pro	
			260					265					270			
Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr	Pro	Leu	Gln	Ala	Thr	Ala	Tyr	Gly	
	275						280					285				
Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu	Leu	Arg	Glu	Ile	
	290					295					300					
Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala	Gly	Glu	Ser	Glu	
305					310					315					320	
Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu	Asn	Thr	Asn	
			325						330					335		
Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu	Tyr	Gly	Trp	
			340					345					350			
Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala	Asn	Gln	Asp	
	355						360					365				
Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu	Gly	Phe	Pro	
	370					375					380					
Ala	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu	Gly	Phe	Leu	Asp	
385					390					395					400	
Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala	Ala	Phe	Gly	
			405						410					415		
Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala	Gly	Gly	Arg	
			420					425					430			

Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro	Pro	Phe	Arg
		435					440				445				
Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe	Pro	Lys	Gly
		450				455					460				
Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu	Asn	Cys	Thr
465					470					475					480
Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp	Leu	Ala	Thr
			485						490					495	
Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu	Tyr	Thr	Leu
			500					505					510		
Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg	Thr	Thr	Gly
		515					520					525			
Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala	Asn	Asp	Gly
		530				535					540				
Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr	Leu	Glu	Glu
545					550					555					560
Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu	Gly	Ala	Tyr
			565						570					575	
Pro	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp	Gln	Ile	Ala	Ala
			580					585					590		
Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile	Val	Ala	Gln
		595					600					605			
Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr	Tyr	Asn	Ala
		610				615					620				
Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val	Tyr	His	Ser
625					630					635					640
Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala	Ser	Ala	Thr
			645						650					655	
Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala	Trp	Ala	Ala
			660					665					670		
Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys	Gln	Val	Pro	Asn
		675					680					685			
Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val	Asp	Val	Ser
		690				695					700				
Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg	Tyr	Tyr	Thr
705					710					715					720
Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Ser	Gly	Gly
			725						730					735	
Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val
			740					745					750		
Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala
		755					760					765			
Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys
		770				775					780				
Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu
785					790					795					800
Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu
			805						810					815	
Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn
			820					825					830		
Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly
		835					840					845			
Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu

850						855										860
Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	
865					870					875					880	
Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	
				885						890				895		
Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	
			900					905					910			
Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	
		915					920					925				
Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	
	930					935					940					
Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	
945					950					955					960	
Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	
				965					970					975		
His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	
		980						985					990			
Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	
		995					1000						1005			
Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	
	1010					1015					1020					
Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	
1025					1030					1035					1040	
Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	
				1045					1050					1055		
Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	
			1060					1065					1070			
Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	
	1075					1080						1085				
Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	
	1090					1095					1100					
Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	
1105					1110					1115					1120	
Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	
				1125					1130					1135		
Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	
			1140					1145					1150			
Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	
	1155						1160					1165				
His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	
	1170					1175					1180					
Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	
1185					1190					1195					1200	
Leu	Val	Pro	Ala	Ala												
				1205												

<210> 30
 <211> 3591
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Nucleotide sequence for a GST:BEST1:K:trAPAO
fusion for bacterial expression in a pGEX-4T-1 or
similar vector

<221> misc_feature
<222> (1)...(687)
<223> gst + polylinker

<221> mat_peptide
<222> (688)...(2163)
<223> BEST1 mature

<221> misc_feature
<222> (2164)...(2199)
<223> spacer sequence

<221> misc_feature
<222> (2200)...(3588)
<223> K:trAPAO

<221> CDS
<222> (1)...(3588)

<221> misc_feature
<222> (2200)...(2202)
<223> Extra lysine

<400> 30

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336

Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
			100					105					110				
aaa	gac	ttt	gaa	act	ctc	aaa	ggt	gat	ttt	ctt	agc	aag	cta	cct	gaa	384	
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
		115					120					125					
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat	432	
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
		130				135					140						
ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat	480	
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
145					150					155					160		
ggt	ggt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta	528	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
				165				170						175			
ggt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac	576	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180				185						190				
ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc	624	
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
acg	ttt	ggt	ggt	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	ggt	ccg	cgt	672	
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
	210					215					220						
gga	tcc	ccg	gaa	ttc	acg	gat	ttt	ccg	gtc	cgc	agg	acc	gat	ctg	ggc	720	
Gly	Ser	Pro	Glu	Phe	Thr	Asp	Phe	Pro	Val	Arg	Arg	Thr	Asp	Leu	Gly		
225					230				235					240			
cag	ggt	cag	gga	ctg	gcc	ggg	gac	gtg	atg	agc	ttt	cgc	gga	ata	ccc	768	
Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg	Gly	Ile	Pro		
			245					250					255				
tat	gca	gcg	ccg	ccg	gtg	ggc	ggg	ctg	cgt	tgg	aag	ccg	ccc	caa	cac	816	
Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro	Pro	Gln	His		
			260					265					270				
gcc	cgg	ccc	tgg	gcg	ggc	ggt	cgc	ccc	gcc	acc	caa	ttt	ggc	tcc	gac	864	
Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe	Gly	Ser	Asp		
		275					280					285					
tgc	ttc	ggc	gcg	gcc	tat	ctt	cgc	aaa	ggc	agc	ctc	gcc	ccc	ggc	gtg	912	
Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala	Pro	Gly	Val		
	290					295					300						
agc	gag	gac	tgt	ctt	tac	ctc	aac	gta	tgg	gcg	ccg	tca	ggc	gct	aaa	960	
Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser	Gly	Ala	Lys		

305		310		315		320	
ccc ggc cag tac	ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc	1008					
Pro Gly Gln Tyr	Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala						
	325 330 335						
ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga	1056						
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg							
	340 345 350						
cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac atc ctg ggc	1104						
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly							
	355 360 365						
ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg	1152						
Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser							
	370 375 380						
ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag	1200						
Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln							
	385 390 395 400						
agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt	1248						
Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe							
	405 410 415						
ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg	1296						
Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro							
	420 425 430						
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg	1344						
Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu							
	435 440 445						
acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg ggc gag cgc	1392						
Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ser Gly Glu Arg							
	450 455 460						
ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg	1440						
Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu							
	465 470 475 480						
atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac ctg cgc agg	1488						
Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg							
	485 490 495						
ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc	1536						
Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr							
	500 505 510						
gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg	1584						
Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu							
	515 520 525						

atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg cgc gcg ccg Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro 530 535 540	1632
atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt ggc Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly 545 550 555 560	1680
gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac ggc cgg gcc Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala 565 570 575	1728
acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat cag ttc aat Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn 580 585 590	1776
cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag ggc gcg ccc Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro 595 600 605	1824
gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga aga gcg ccg Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro 610 615 620	1872
gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu 625 630 635 640	1920
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala 645 650 655	1968
gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala 660 665 670	2016
aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser 675 680 685	2064
acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc gcg gcg gtg Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val 690 695 700	2112
gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc gcc aag gcg Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala 705 710 715 720	2160
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn 725 730 735	2208

gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg	2256
Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr	
740 745 750	
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg	2304
Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala	
755 760 765	
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc	2352
Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly	
770 775 780	
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac	2400
Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn	
785 790 795 800	
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag	2448
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu	
805 810 815	
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca	2496
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr	
820 825 830	
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca	2544
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala	
835 840 845	
agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag	2592
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu	
850 855 860	
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac	2640
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp	
865 870 875 880	
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct	2688
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala	
885 890 895	
gtt ctc ggc gta gca aac cag atc aca gcg gct ctg ctc ggt gtg gaa	2736
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu	
900 905 910	
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc	2784
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala	
915 920 925	
acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat	2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr	
930 935 940	
atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag	2880

Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	
945					950					955					960	
gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att																2928
Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	
				965					970					975		
gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg																2976
Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	
			980					985					990			
ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc																3024
Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	
			995				1000					1005				
acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg																3072
Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	
	1010						1015				1020					
gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac																3120
Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	
1025					1030					1035					1040	
aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc																3168
Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	
				1045					1050					1055		
tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga																3216
Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	
			1060					1065					1070			
caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg																3264
Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	
			1075				1080					1085				
tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc																3312
Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	
	1090						1095					1100				
cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac																3360
Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	
1105					1110					1115					1120	
gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg																3408
Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	
				1125					1130					1135		
agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc																3456
Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	
			1140					1145					1150			
aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta																3504
Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	

1155	1160	1165	
gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt			3552
Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly			
1170	1175	1180	
gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			3591
Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
1185	1190	1195	

<210> 31
 <211> 1196
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Translation of the GST:BEST1:K:trAPAO fusion
 sequence for bacterial expression as provided in
 SEQ ID NO: 30

<400> 31

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
1				5				10						15	
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
			20					25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35					40					45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50					55					60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70					75					80
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90					95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100					105					110		
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
		115					120					125			
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
		130					135					140			
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145					150					155					160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165					170					175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
			180					185					190		
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195					200					205			
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210				215						220				
Gly	Ser	Pro	Glu	Phe	Thr	Asp	Phe	Pro	Val	Arg	Arg	Thr	Asp	Leu	Gly
225					230					235					240
Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg	Gly	Ile	Pro

				245					250					255			
Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro	Pro	Gln	His		
			260					265					270				
Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe	Gly	Ser	Asp		
		275					280					285					
Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala	Pro	Gly	Val		
	290					295					300						
Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser	Gly	Ala	Lys		
305					310					315					320		
Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly	Gly	Phe	Ala		
				325					330					335			
Gly	Gly	Thr	Ala	Ala	Met	Pro	Tyr	Tyr	Asp	Gly	Glu	Ala	Leu	Ala	Arg		
			340					345					350				
Gln	Gly	Val	Val	Val	Val	Thr	Phe	Asn	Tyr	Arg	Thr	Asn	Ile	Leu	Gly		
		355					360					365					
Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr	Gly	Thr	Ser		
	370					375					380						
Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg	Trp	Val	Gln		
385					390					395					400		
Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val	Thr	Val	Phe		
				405					410					415			
Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu	Thr	Ser	Pro		
			420					425					430				
Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	Pro	Gly	Leu		
		435					440					445					
Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	Gly	Glu	Arg		
	450					455					460						
Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	Ala	Thr	Leu		
465					470					475					480		
Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp	Leu	Arg	Arg		
				485					490					495			
Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	Pro	Gln	Thr		
			500					505					510				
Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	Arg	Val	Leu		
		515					520					525					
Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro		
	530					535					540						
Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	Gln	Phe	Gly		
545					550					555					560		
Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	Gly	Arg	Ala		
				565					570					575			
Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn		
			580					585					590				
Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	Gly	Ala	Pro		
		595					600					605					
Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	Arg	Ala	Pro		
	610					615					620						
Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	Phe	Lys	Leu		
625					630					635					640		
Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala		
				645					650					655			
Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	Arg	Phe	Ala		
			660					665					670				

Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	Ala	Tyr	Ser	675	680	685
Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	Ala	Ala	Val	690	695	700
Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	Ala	Lys	Ala	705	710	715
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	720	725	730
Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	735	740	745
Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	750	755	760
Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	765	770	775
Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	780	785	790
Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	795	800	805
Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	810	815	820
Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	825	830	835
Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	840	845	850
His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	855	860	865
Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	870	875	880
Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	885	890	895
Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	900	905	910
Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	915	920	925
Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	930	935	940
Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	945	950	955
Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	960	965	970
Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	975	980	985
Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	990	995	1000
Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	1005	1010	1015
Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	1020	1025	1030
Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	1035	1040	1045
Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	1050	1055	1060
Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	1065	1070	1075

```

      1090              1095              1100
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn
1105              1110              1115              1120
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro
      1125              1130              1135
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu
      1140              1145              1150
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu
      1155              1160              1165
Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
      1170              1175              1180
Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
1185              1190              1195

```

```

<210> 32
<211> 2490
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GST:glyc(-)APAO open reading frame

```

```

<221> CDS
<222> (1)...(2487)

<221> misc_feature
<222> (1)...(687)
<223> GST and linker

```

```

<221> misc_feature
<222> (688)...(2490)
<223> Glyc (-) APAO

```

```

<221> mutation
<222> (1288)...(1290)
<223> mutation in putative glycosylation site (AAT->TCC)

```

```

<221> mutation
<222> (1303)...(1305)
<223> mutation in putative glycosylation site (AGC->AAC)

```

```

<400> 32
atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc   48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1              5              10              15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg   96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20              25              30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg   144

```

Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
		35					40					45					
ggt	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggt	gat	gtt	aaa	192	
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
	50					55					60						
tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac	240	
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
	65				70					75					80		
atg	ttg	ggt	ggt	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	288	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
				85				90						95			
gga	gcg	gtt	ttg	gat	att	aga	tac	ggt	gtt	tcg	aga	att	gca	tat	agt	336	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
			100					105					110				
aaa	gac	ttt	gaa	act	ctc	aaa	gtt	gat	ttt	ctt	agc	aag	cta	cct	gaa	384	
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
		115						120				125					
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat	432	
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
	130					135					140						
ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat	480	
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
	145				150					155					160		
gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta	528	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
				165				170						175			
gtt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac	576	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180					185					190				
ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc	624	
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
acg	ttt	ggt	ggt	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	gtt	ccg	cgt	672	
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
	210					215					220						
gga	tcc	ccg	gaa	ttc	atg	gca	ctt	gca	ccg	agc	tac	atc	aat	ccc	cca	720	
Gly	Ser	Pro	Glu	Phe	Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro		
	225				230					235					240		
aac	gtc	gcc	tcc	cca	gca	ggg	tat	tct	cac	gtc	ggc	gta	ggc	cca	gac	768	
Asn	Val	Ala	Ser	Pro	Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp		

245				250				255				
gga ggg agg tat gtg aca ata gct gga cag att gga caa gac gct tcg	816											
Gly Gly Arg Tyr Val Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser												
260 265 270												
ggc gtg aca gac cct gcc tac gag aaa cag gtt gcc caa gca ttc gcc	864											
Gly Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala												
275 280 285												
aat ctg cga gct tgc ctt gct gca gtt gga gcc act tca aac gac gtc	912											
Asn Leu Arg Ala Cys Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val												
290 295 300												
acc aag ctc aat tac tac atc gtc gac tac gcc ccg agc aaa ctc acc	960											
Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr												
305 310 315 320												
gca att gga gat ggg ctg aag gct acc ttt gcc ctt gac agg ctc cct	1008											
Ala Ile Gly Asp Gly Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro												
325 330 335												
cct tgc acg ctg gtg cca gtg tcg gcc ttg tct tca cct gaa tac ctc	1056											
Pro Cys Thr Leu Val Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu												
340 345 350												
ttt gag gtt gat gcc acg gcg ctg gtg ccg gga cac acg acc cca gac	1104											
Phe Glu Val Asp Ala Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp												
355 360 365												
aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag	1152											
Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu												
370 375 380												
acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag	1200											
Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu												
385 390 395 400												
gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc	1248											
Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro												
405 410 415												
ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc tcc gac agc	1296											
Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Ser Asp Ser												
420 425 430												
aac caa aac gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc	1344											
Asn Gln Asn Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly												
435 440 445												
gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt	1392											
Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly												
450 455 460												

aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt	1440
Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val	
465 470 475 480	
gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa	1488
Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu	
485 490 495	
gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc	1536
Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu	
500 505 510	
gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct	1584
Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro	
515 520 525	
gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg	1632
Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val	
530 535 540	
gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt	1680
Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser	
545 550 555 560	
gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag	1728
Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln	
565 570 575	
tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca	1776
Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser	
580 585 590	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa	1824
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu	
595 600 605	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc	1872
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
610 615 620	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat	1920
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
625 630 635 640	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	1968
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
645 650 655	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg	2016
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	
660 665 670	

gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg	2064
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
675 680 685	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	2112
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp	
690 695 700	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag	2160
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys	
705 710 715 720	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa	2208
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln	
725 730 735	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc	2256
Leu Arg Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala	
740 745 750	
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct	2304
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala	
755 760 765	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg	2352
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala	
770 775 780	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct	2400
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser	
785 790 795 800	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga	2448
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg	
805 810 815	
ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	2490
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
820 825	

<210> 33

<211> 829

<212> PRT

<213> Artificial Sequence

<220>

<223> Translation of SEQ ID NO: 32 showing sequence of GST:APAO in which 2 APAO amino acids have been changed by site-directed mutagenesis to eliminate 2 potential glycosylation sites

<400> 33

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
1				5					10					15	
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
			20					25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35					40					45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50					55					60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70					75				80	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85				90						95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100					105					110		
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
		115					120					125			
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130					135					140				
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145					150					155				160	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165				170						175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
			180					185					190		
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195					200					205			
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210				215						220				
Gly	Ser	Pro	Glu	Phe	Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro
225					230					235				240	
Asn	Val	Ala	Ser	Pro	Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp
				245					250					255	
Gly	Gly	Arg	Tyr	Val	Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser
			260					265					270		
Gly	Val	Thr	Asp	Pro	Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala
		275					280					285			
Asn	Leu	Arg	Ala	Cys	Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val
	290					295					300				
Thr	Lys	Leu	Asn	Tyr	Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr
305					310					315				320	
Ala	Ile	Gly	Asp	Gly	Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro
				325					330					335	
Pro	Cys	Thr	Leu	Val	Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu
			340					345					350		
Phe	Glu	Val	Asp	Ala	Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp
		355					360					365			
Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu
	370					375					380				
Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu
385					390					395				400	
Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro
				405					410					415	
Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Ser	Asp	Ser

<210> 34
<211> 11
<212> PRT
<213> *Exophiala spinifera*

<220>
<221> BINDING
<222> (0)...(0)
<223> Amino-terminal dinucleotide (ADP) binding region
of trAPAO amino oxidase domain, characterized by a
beta-alpha-beta stretch containing 3 invariant
glycines (GXGXXG) in the beta-alpha turn.

<400> 34
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10

<210> 35
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Example spacer sequence

<400> 35
Gly Gly Gly Ser Gly Gly Gly Ser
1 5